WHAT IS CLAIMED IS:

1. A method for analysis of proteins in a biological system comprising:

providing a biological system;

exposing the system to a stimulus;

sampling the biological system at multiple time intervals after exposing the system to the stimulus,

treating the multiple samples by separation technique to provide multiple protein samples suitable for analysis by mass spectrometry, and

analyzing the multiple samples to determine changes in protein abundance as a function of time after exposing the biological system to stimulus, said analyzing including

providing a parallel array of mass spectrometry systems adapted for protein analysis, and

directing mass spectral data from the mass spectrometry systems in said array to a common computing device, said mass spectral data being indicative of the identity and the abundance of protein in said multiple sample, and

correlating said mass spectral data as a function of time.

2. The method of claim 1 comprising displaying said correlated data as a function of protein identity, protein abundance, and time.

3. The method of claim 1 wherein the correlated data is stored in a searchable database.

4. The method of claim 1 comprising identifying proteins based on changes in abundance as a function of time.

5. The method of claim 4 wherein said array includes at least 20 mass spectrometers.

6. The method of claim 4 comprising analyzing 500 proteins or more.

7. The method of claim 6 comprising analyzing 5000 proteins or more.

8. The method of claim 4 wherein the separation technique includes separation apparatus and said common computing device communicates with said separation apparatus.

9. The method of claim 8 wherein the separation technique includes chromatography.

10. The method of claim 8 wherein the separation technique includes use of a magnetic particle separation apparatus.

11. The method of claim 10 where the magnetic particle separation apparatus treats multiple samples in parallel.

12. The method of claim 4 wherein said mass spectral data includes peptide fragment mass spectra and an amino acid sequence derived from a data base.

13. The method of claim 12 wherein said mass spectrometer are LC-TMS mass spectrometers.

14. The method of claim 4 comprising

exposing a first component of the biological system to a stimulus and maintaining a second component of the biological system free of the stimulus,

sampling and analyzing each of the first component and the second component and comparing the identity and abundance in the first component and the second component.

15. The method of claim 14 comprising separately analyzing samples from said first component and second component.

16. The method of claim 4 wherein the stimulus is a drug.

17. The method of claim 4 wherein the time interval is about 5 to 60 seconds.

18. The method of claim 4 wherein the time interval is about one minute to one hour.

19. A system for mass spectrometric analysis comprising:

a parallel sample separation apparatus adapted to separate multiple samples in parallel for analysis by mass spectrometry, and

a parallel array of mass spectrometry systems adapted to receive the samples from the separation apparatus, and

a common computing device communicating with the parallel array of mass spectrometry systems and the parallel separation apparatus, the common computing device being adapted to analyze mass spectral data from the parallel array of mass spectrometry systems as function of sample identity.

20. The system of claim 19 where the parallel separation device is a parallel magnetic particle separation device.

21. The system of claim 19 wherein said array includes at least 2 mass spectrometers.

22. A method for analysis of proteins in a biological system comprising:

providing a biological system containing proteins;

exposing the biological system to a stimulus;

after exposing the biological system to the stimulus, sampling the biological system at multiple time intervals to obtain multiple samples;

treating the multiple samples by a separation technique to provide multiple protein samples suitable for analysis by mass spectrometry;

providing a parallel array of mass spectrometer systems capable of simultaneous analysis of as many protein samples as there are spectrometer systems in said array;

analyzing the multiple protein samples in said parallel array of mass spectrometry systems to generate mass spectral data indicative of the identity and the abundance of proteins in said multiple protein samples; and

in a common electronic computing device communicating with each of said mass spectrometry systems, correlating said mass spectral data as a function of time.

23. The system of claim 22 where the parallel separation device is a parallel magnetic particle separation device.

24. The system of claim 23 wherein the parallel array includes an array of LC-MS spectrometer system.

25. The system of claim 24 wherein the array includes 6-20 mass spectrometers.

26. The system of claim 25 wherein the time intervals are in the range of 5 seconds to 10 minutes.

27. The system of claim 26 wherein the analysis includes analysis of about 500 proteins or more.

28. The method of claim 27 wherein the central computer communicates with the separation.

APPENDIX:

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